

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/554,246
Source: PCF
Date Processed by STIC: 1/16/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED
SUGGESTED CORRECTION
SERIAL NUMBER:

10/554,246

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|---------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1 | ____ Wrapped Nucleic
____ Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | ____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | ____ Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. |
| 4 | ____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | ____ Variable Length | Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | ____ PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | ____ Skipped Sequences
(OLD RULES) | Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | ____ Skipped Sequences
(NEW RULES) | Sequence(s) ____ missing. If intentional , please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | ____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 | ____ Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | ____ Use of <220> | Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | ____ PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | V Misuse of n/Xaa | "n" can only represent a single <u>nucleotide</u> ; " <u>Xaa</u> " can only represent a single <u>amino acid</u> |



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/554,246

DATE: 01/16/2007
TIME: 14:43:00

Input Set : A:\OKAD3006 Sequence Listing.ST25.txt
Output Set: N:\CRF4\01162007\J554246.raw

3 <110> APPLICANT: OZAWA, Keiya
 4 OKADA, Takashi
 6 <120> TITLE OF INVENTION: Gene Introduction Efficiency Enhancer
 8 <130> FILE REFERENCE: OKAD3006/GAL
 10 <140> CURRENT APPLICATION NUMBER: 10/554,246
 11 <141> CURRENT FILING DATE: 2005-10-25
 13 <150> PRIOR APPLICATION NUMBER: JP2003-122968
 14 <151> PRIOR FILING DATE: 2003-04-25
 16 <160> NUMBER OF SEQ ID NOS: 1
 18 <170> SOFTWARE: PatentIn version 3.3
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 4
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Chromobacterium sp.
 26 <220> FEATURE:
 27 <221> NAME/KEY: SITE
 28 <222> LOCATION: (1)..(1)
 29 <223> OTHER INFORMATION: In the formula COOHCH₂CH(CHCH₂H₄SH) OH, the carboxylic group

is

30 bonded with the amino group of the first amino acid Val.

32 <220> FEATURE:

33 <221> NAME/KEY: SITE

34 <222> LOCATION: (2)..(2)

35 <223> OTHER INFORMATION: In the formula COOHCH₂CH(CHCH₂H₄SH) OH, the SH group is bonded

36 with the SH group of the second amino acid Cys via a disulfide bond.

39 <220> FEATURE:

40 <221> NAME/KEY: SITE

41 <222> LOCATION: (3)..(3)

42 <223> OTHER INFORMATION: Xaa is an amino acid represented by the formula NH₂C(CHCH₃)₂

COOH.

44 <220> FEATURE:

45 <221> NAME/KEY: SITE

46 <222> LOCATION: (4)..(4)

47 <223> OTHER INFORMATION: In the formula COOHCH₂CH(CHCH₂H₄SH) OH, the hydroxyl group is bonded with the carboxylic group of the fourth amino acid Val.

50 <400> SEQUENCE: 1

W--> 52 Val Cys Xaa Val

53 1

Dose Not Comply
Corrected Diskette Needed

(pg. 1)

✓ See item #13 on error summary sheet.

INVALID Response

Xaa can only represent
a single amino Acid.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/16/2007
PATENT APPLICATION: US/10/554,246 TIME: 14:43:01

Input Set : A:\OKAD3006 Sequence Listing.ST25.txt
Output Set: N:\CRF4\01162007\J554246.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 3

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/554,246

DATE: 01/16/2007

TIME: 14:43:01

Input Set : A:\OKAD3006 Sequence Listing.ST25.txt

Output Set: N:\CRF4\01162007\J554246.raw

L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0